

EXHIBIT 2

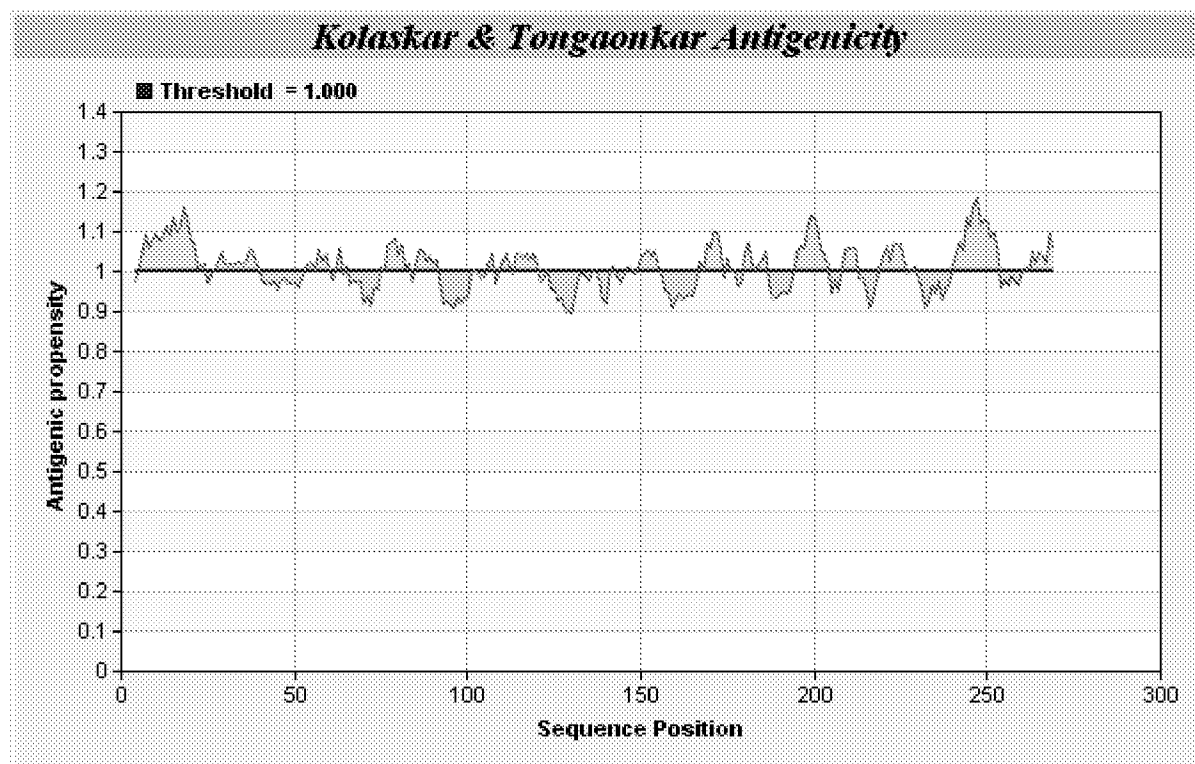
IEDB Analysis Resource

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Kolaskar & Tongaonkar Antigenicity

Sequence:

```
1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST MQQASYAMGV
61 DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH
121 KADAKANKEK GEAPLKENAA KDGVKTTASG LQYKITKQGE GKQPTKDDIV TVEYEGRLID
181 GTVFDSSKAN GGPATFPLSQ VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN
241 ATLVFDVKLV KIGAPENAPA KPDQQVDIKK VN
```

Center position: 4 Window size: 7**Average: 1.010 Minimum: 0.897 Maximum: 1.184 Threshold: 1.000**[Click here to view plotted values in table format](#)

Predicted peptides:

No.	Start Position	End Position	Peptide	Peptide Length
1	5	24	FKISALTLSAALALSACGKK	20

2	27	39	APASASEPAAASA	13
3	53	60	QASYAMGV	8
4	77	83	DLKVFTD	7
5	85	91	MQAVYDG	7
6	114	120	AKAVEKH	7
7	149	155	SGLQYKI	7
8	167	173	DDIVTVE	7
9	180	186	DGTVFDS	7
10	195	204	TFPLSQVIPG	10
11	219	226	TFYIPSNL	8
12	240	253	NATLVFDVKLVKIG	14

Reference: Kolaskar AS, Tongaonkar PC. A semi-empirical method for prediction of antigenic determinants on protein antigens. FEBS Lett. 1990 Dec 10;276(1-2):172-4.

Scale values: A:1.064, C:1.412, D:0.866, E:0.851, F:1.091, G:0.874, H:1.105, I:1.152, K:0.93, L:1.25, M:0.826, N:0.776, P:1.064, Q:1.015, R:0.873, S:1.012, T:0.909, V:1.383, W:0.893, Y:1.161